

09/647019  
430 Rec'd PTO 26 SEP 2000

WO 99/50410

PCT/AU99/00220

- 1 -

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: THE VICTOR CHANG CARDIAC  
RESEARCH INSTITUTE, THE  
GENERAL HOSPITAL CORPORATION and  
THE WALTER AND ELIZA HALL  
INSTITUTE OF MEDICAL RESEARCH.
- (ii) TITLE OF INVENTION: NOVEL THERAPEUTIC MOLECULES  
AND USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: DAVIES COLLISON CAVE  
(B) STREET: 1 LITTLE COLLINS STREET  
(C) CITY: MELBOURNE  
(D) STATE: VICTORIA  
(E) COUNTRY: AUSTRALIA  
(F) ZIP: 3000
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: INTERNATIONAL APPLICATION  
(B) FILING DATE: 26-MAR-1999  
(C) CLASSIFICATION:
- (vii) PREVIOUS APPLICATION DATA:  
(A) APPLICATION NUMBER: PP2634/98  
(B) FILING DATE: 27-MAR-1998
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: HUGHES, DR E JOHN L  
(C) REFERENCE/DOCKET NUMBER: EJH/TDO/DK
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: +61 3 9254 2777  
(B) TELEFAX: +61 3 9254 2770  
(C) TELEX: AA 31787

09647019-013604

WO 99/50410

PCT/AU99/00220

- 2 -

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 778 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 199..453
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTCTCAGGA CTGGAGAGAG ACAGAGCACT CCAGCTATTT CAGCCACATG AAAAGCACTG 60  
 GAATTGAGAT CCCCCGCTCAG AGGACACCGG GAGTTCCTTC TATCCTGTAA AGCGCTTTTTT 120  
 GTGTTTTTGC ACCTGGCCCG CTGGGACTGT CCTCAGGCAG TAAACCAATC CAGAGAGCAG 180  
 GGCTAAGACC TTGTGAAT ATG TCG AAG CAG CCA ATT TCC AAC GTC AGA GCC 231  
                   Met Ser Lys Gln Pro Ile Ser Asn Val Arg Ala  
                           1                  5                          10

ATC CAG GCG AAT ATC AAT ATT CCA ATG GGA GCC TTT CGT CCG GGA GCT 279  
 Ile Gln Ala Asn Ile Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala  
                   15                  20                          25

GGG CAG CCT CCC AGA AGG AAA GAG AGT ACT CCT GAA ACT GAG GAG GGA 327  
 Gly Gln Pro Pro Arg Arg Lys Glu Ser Thr Pro Glu Thr Glu Glu Gly  
                   30                          35                          40

GCT CCT ACC ACC TCA GAG GAA AAG AAG CCA ATT CCT GGA ATG AAG AAA 375  
 Ala Pro Thr Thr Ser Glu Glu Lys Lys Pro Ile Pro Gly Met Lys Lys  
                   45                          50                          55

TTT CCA GGA CCT GTT GTC AAC TTG TCT GAG ATC CAA AAT GTT AAA AGT 423  
 Phe Pro Gly Pro Val Val Asn Leu Ser Glu Ile Gln Asn Val Lys Ser  
                   60                          65                          70                          75

GAA CTG AAA TTT GTC CCC AAA GGT GAA CAG TAGTCGAAAG GACACAAAAG 473  
 Glu Leu Lys Phe Val Pro Lys Gly Glu Gln  
                           80                          85

TTCACATTGG ATGCTTAGAA TCAGGAGATG CATTTCTGTTG ACGTGTTTTTT CCAAGGGAGA 533  
 AAAAAAATG GGTGAAATA AACAACTTCC TGAACATTTT ATACATTTGT ATGATGATCA 593  
 CAAACCTCCT GAATGCCCAA GACTCTAGCA AAAATATCCT GTTGTGTACAT TTATATTCT 653  
 TCCTTTTACT TGGTTGCATT TCTCACTTTA GCTACATTTT TGGCACCTTG TAGAGCAAAT 713  
 CAGCACACGA ATTTACAACC TGGGAAGTGT GGTTTTGAGG AGAGATGTGA TTTTATGAA 773  
 GGGGG 778

09647015-012601

WO 99/50410

PCT/AU99/00220

- 3 -

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 85 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Ser Lys Gln Pro Ile Ser Asn Val Arg Ala Ile Gln Ala Asn Ile
 1           5           10           15
Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln Pro Pro Arg
          20           25           30
Arg Lys Glu Ser Thr Pro Glu Thr Glu Glu Gly Ala Pro Thr Thr Ser
          35           40           45
Glu Glu Lys Lys Pro Ile Pro Gly Met Lys Lys Phe Pro Gly Pro Val
          50           55           60
Val Asn Leu Ser Glu Ile Gln Asn Val Lys Ser Glu Leu Lys Phe Val
          65           70           75           80
Pro Lys Gly Glu Gln
                  85

```

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 887 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 185..448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

GGTTCTCAAT ACCGGGAGAG GCACAGAGCT ATTTGAGCCA CATGAAAAGC ATCGGAATTG      60
AGATCGCAGC TCAGAGGACA CCGGGCGCCC CTTCCACCTT CCAAGGAGCT TTGTATTCTT      120
GCATCTGGCT GCCTGGGACT TCCCTTAGGC AGTAAACAAA TACATAAAGC AGGGATAAGA      180
CTGC ATG AAT ATG TCG AAA CAG CCA GTT TCC AAT GTT AGA GCC ATC CAG      229
  Met Asn Met Ser Lys Gln Pro Val Ser Asn Val Arg Ala Ile Gln
    1           5           10           15
GCA AAT ATC AAT ATT CCA ATG GGA GCC TTT CGG CCA GGA GCA GGT CAA      277
Ala Asn Ile Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln
          20           25           30
CCC CCC AGA AGA AAA GAA TGT ACT CCT GAA GTG GAG GAG GGT GTT CCT      325
Pro Pro Arg Arg Lys Glu Cys Thr Pro Glu Val Glu Glu Gly Val Pro
          35           40           45

```

T092709"043604

**PCT/AU99/00220**

**0968-7621**

Lys Tyr Val Pro Lys Ala Glu Gln  
85

WO 99/50410

PCT/AU99/00220

- 5 -

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 75 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Met Ser Lys Gln Pro Ala Ser Asn Ile Arg Ser Ile Gln Ala Asn Ile
1           5           10           15
Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln Pro Pro Lys
                20           25           30
Arg Lys Glu Phe Ser Thr Glu Glu Glu Gln His Val Pro Thr Pro Glu
                35           40           45
Ser Glu Glu Lys Ser Glu Glu Lys Lys Pro Ile Pro Gly Ala Val Lys
                50           55           60
Leu Pro Gly Pro Ala Phe Asn Leu Ser Glu Thr
65           70           75

```

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 887 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

GGTTCTCAAT ACCGGGAGAG GCACAGAGCT ATTTCAGCCA CATGAAAAGC ATCGGAATTG      60
AGATCGCAGC TCAGAGGACA CCGGGCGCCC CTTCCACCTT CCAAGGAGCT TTGTATTCTT      120
GCATCTGGCT GCCTGGGACT TCCCTTAGGC AGTAAACAAA TACATAAAGC AG      172

```

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 887 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

GGATAAGACT GCATGAATAT GTCGAAACAG CCAGTTTCCA ATGTTAGAGC CATCCAG      57

```

09647019.042601

WO 99/50410

PCT/AU99/00220

- 6 -

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 887 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCAAATATCA ATATTCCAAT GGGAGCCTTT CGGCCAGGAG CAGGTCAACC CCCCAGAAGA	60
AAAGAATGTA CTCCTGAAGT GGAGGAG	87

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 887 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGTGTTCCTC CCACCTCGGA TGAGGAGAAG AAGCCAATTC CAGGAGCGAA GAAACTTCCA	60
GGACCTGCAG TCAATCTATC GGAAATCCAG AATATTAAAA GTGAACTAAA ATATGTCCCC	120
AAAGCTGAAC AGTAGTAGGA AGAAAAAAG	149

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 887 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATTGATGTG AAGAAATAAA GAGGCAGAAG ATGGATTCAA TAGCTCACTA AAATTTTATA	60
TATTTGTATG ATGATTGTGA ACCTCCTGAA TGCCTGAGAC TCTAGCAGAA ATGGCCTGTT	120
TGTACATTTA TATCTCTTCC TTCTAGTTGG CTGTATTTCT TACTTTTATCT TCATTTTGGG	180
CACCTCACAG AACAAATTAG CCCATAAATT CAACACCTGG AGGGTGTGGT TTTGAGGAGG	240
GATATGATTT TATGGAGAAT GATATGGCAA TGTGCCTAAC GATTTTGATG AAAAGTTTCC	300
CAAGCTACTT CCTACAGTAT TTTGGTCAAT ATTTGGAATG CGTTTTAGTT CTTACCTTTT	360
TAAATTATGT CACTAAACTT TGTATGAGTT CAAATAAATA TTTGACTAAA TGTAAAAATGT	420
GA	422

09647049.012601

## SEQUENCE LISTING

<110> Harvey, Richard P.  
Palmer, Stephen J.  
Rosenthal, Nadia A.  
Musaro, Antonio

<120> NOVEL MOLECULES EXPRESSED DURING MUSCLE  
DEVELOPMENT AND GENETIC SEQUENCES ENCODING THE SAME

<130> 12525-407001

<140> 09/647,019

<141> 2000-09-26

<150> PCT/AU99/00220

<151> 1999-03-26

<150> AU PP2634/98

<151> 1998-03-27

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 778

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (199)...(453)

<400> 1

```

gctctcagga ctggagagag acagagcact ccagctatatt cagccacatg aaaagcactg      60
gaattgagat ccccgctcag aggacaccgg gagttccttc taccctgtaa agcgcttttt      120
gtgtttttgc acctggccgc ctgggactgt cctcaggcag taaaccaatc cagagagcag      180
ggctaagacc ttgtgaat atg tgc aag cag cca att tcc aac gtc aga gcc      231
                Met Ser Lys Gln Pro Ile Ser Asn Val Arg Ala
                  1                5                10

atc cag gcg aat atc aat att cca atg gga gcc ttt cgt ccg gga gct      279
Ile Gln Ala Asn Ile Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala
                15                20                25

ggg cag cct ccc aga agg aaa gag agt act cct gaa act gag gag gga      327
Gly Gln Pro Pro Arg Arg Lys Glu Ser Thr Pro Glu Thr Glu Glu Gly
                30                35                40

gct cct acc acc tca gag gaa aag aag cca att cct gga atg aag aaa      375
Ala Pro Thr Thr Ser Glu Glu Lys Lys Pro Ile Pro Gly Met Lys Lys
                45                50                55

ttt cca gga cct gtt gtc aac ttg tct gag atc caa aat gtt aaa agt      423

```

09647019-013601

Phe Pro Gly Pro Val Val Asn Leu Ser Glu Ile Gln Asn Val Lys Ser  
60 65 70 75

gaa ctg aaa ttt gtc ccc aaa ggt gaa cag tagtcgaaag gacacaaaag 473  
Glu Leu Lys Phe Val Pro Lys Gly Glu Gln  
80 85

ttcacattgg atgcttagaa tcaggagatg catttcgttg acgtgttttt ccaagggaga 533  
aaaaacaatg ggttgaaata aacaacttcc tgaacatttt atacatttgt atgatgatca 593  
caaacctcct gaatgcccaa gactctagca aaaatatacct gtttgtacat ttatatattct 653  
tccttttact tgggtgcatt tctcacttta gctacatttt tggcaccttg tagagcaaat 713  
cagcacacga atttacaacc tgggaagtgt ggttttgagg agagatgtga tttttatgaa 773  
ggggg 778

<210> 2  
<211> 85  
<212> PRT  
<213> Mus musculus

<400> 2  
Met Ser Lys Gln Pro Ile Ser Asn Val Arg Ala Ile Gln Ala Asn Ile  
1 5 10 15  
Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln Pro Pro Arg  
20 25 30  
Arg Lys Glu Ser Thr Pro Glu Thr Glu Glu Gly Ala Pro Thr Thr Ser  
35 40 45  
Glu Glu Lys Lys Pro Ile Pro Gly Met Lys Lys Phe Pro Gly Pro Val  
50 55 60  
Val Asn Leu Ser Glu Ile Gln Asn Val Lys Ser Glu Leu Lys Phe Val  
65 70 75 80  
Pro Lys Gly Glu Gln  
85

<210> 3  
<211> 887  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (185)...(448)

<400> 3  
ggttctcaat accgggagag gcacagagct atttcagcca catgaaaagc atcggaattg 60  
agatcgagc tcagaggaca ccgggcgcc cttccacctt ccaaggagct ttgtattctt 120  
gcatctggct gcctgggact tcccttaggc agtaacaaa tacataaagc agggataaga 180  
ctgc atg aat atg tcg aaa cag cca gtt tcc aat gtt aga gcc atc cag 229  
Met Asn Met Ser Lys Gln Pro Val Ser Asn Val Arg Ala Ile Gln  
1 5 10 15

gca aat atc aat att cca atg gga gcc ttt cgg cca gga gca ggt caa 277  
Ala Asn Ile Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln  
20 25 30

ccc ccc aga aga aaa gaa tgt act cct gaa gtg gag gag ggt gtt cct 325  
Pro Pro Arg Arg Lys Glu Cys Thr Pro Glu Val Glu Glu Gly Val Pro  
35 40 45

09647049.04.2004

ccc acc tcg gat gag gag aag aag cca att cca gga gcg aag aaa ctt 373  
 Pro Thr Ser Asp Glu Glu Lys Lys Pro Ile Pro Gly Ala Lys Lys Leu  
           50                          55                          60

cca gga cct gca gtc aat cta tcg gaa atc cag aat att aaa agt gaa 421  
 Pro Gly Pro Ala Val Asn Leu Ser Glu Ile Gln Asn Ile Lys Ser Glu  
           65                          70                          75

cta aaa tat gtc ccc aaa gct gaa cag tagtaggaag aaaaaaggat 468  
 Leu Lys Tyr Val Pro Lys Ala Glu Gln  
           80                          85

tgatgtgaag aaataaagag gcagaagatg gattcaatag ctactaaaa ttttatatat 528  
 ttgtatgatg attgtgaacc tcctgaatgc ctgagactct agcagaaatg gcctgtttgt 588  
 acatttatat ctcttccttc tagttggctg tatttcttac tttatcttca tttttggcac 648  
 ctcacagaac aaattagccc ataaattcaa cacctggagg gtgtgggtttt gaggagggat 708  
 atgattttat ggagaatgat atggcaatgt gcctaacgat tttgatgaaa agtttcccaa 768  
 gctacttcct acagtatttt ggtcaatatt tggaatgcgt tttagttctt caccttttaa 828  
 attatgtcac taaactttgt atgagttcaa ataaatattt gactaaatgt aaaatgtga 887

<210> 4  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Met Asn Met Ser Lys Gln Pro Val Ser Asn Val Arg Ala Ile Gln Ala  
   1                          5                          10                          15  
 Asn Ile Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln Pro  
           20                          25                          30  
 Pro Arg Arg Lys Glu Cys Thr Pro Glu Val Glu Glu Gly Val Pro Pro  
           35                          40                          45  
 Thr Ser Asp Glu Glu Lys Lys Pro Ile Pro Gly Ala Lys Lys Leu Pro  
           50                          55                          60  
 Gly Pro Ala Val Asn Leu Ser Glu Ile Gln Asn Ile Lys Ser Glu Leu  
   65                          70                          75                          80  
 Lys Tyr Val Pro Lys Ala Glu Gln  
                           85

<210> 5  
 <211> 75  
 <212> PRT  
 <213> Xenopus laevis

<400> 5  
 Met Ser Lys Gln Pro Ala Ser Asn Ile Arg Ser Ile Gln Ala Asn Ile  
   1                          5                          10                          15  
 Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln Pro Pro Lys  
           20                          25                          30  
 Arg Lys Glu Phe Ser Thr Glu Glu Glu Gln His Val Pro Thr Pro Glu  
           35                          40                          45  
 Ser Glu Glu Lys Ser Glu Glu Lys Lys Pro Ile Pro Gly Ala Val Lys  
           50                          55                          60  
 Leu Pro Gly Pro Ala Phe Asn Leu Ser Glu Thr  
   65                          70                          75

09647019.012601

<210> 6  
 <211> 172  
 <212> DNA  
 <213> Homo sapiens

<400> 6  
 gggttctcaat accgggagag gcacagagct atttcagcca catgaaaagc atcggaattg 60  
 agatcgagc tcagaggaca ccgggcgccc cttccacctt ccaaggagct ttgtattctt 120  
 gcatctggct gcctgggact tcccttaggc agtaaacaaa tacataaagc ag 172

<210> 7  
 <211> 57  
 <212> DNA  
 <213> Homo sapiens

<400> 7  
 ggataagact gcatgaatat gtcgaaacag ccagtttcca atgttagagc catccag 57

<210> 8  
 <211> 87  
 <212> DNA  
 <213> Homo sapiens

<400> 8  
 gcaaataatca atattccaat gggagccttt cggccaggag caggtcaacc cccagaaga 60  
 aaagaatgta ctctgaagt ggaggag 87

<210> 9  
 <211> 149  
 <212> DNA  
 <213> Homo sapiens

<400> 9  
 ggtgttcctc ccacctcgga tgaggagaag aagccaattc caggagcgaa gaaacttcca 60  
 ggacctgcag tcaatctatc ggaaatccag aatattaaaa gtgaactaaa atatgtcccc 120  
 aaagctgaac agtagtagga agaaaaaag 149

<210> 10  
 <211> 422  
 <212> DNA  
 <213> Homo sapiens

<400> 10  
 gattgatgtg aagaaataaa gaggcagaag atggattcaa tagctcacta aaattttata 60  
 tatttgtag atgattgtga acctcctgaa tgcctgagac tctagcagaa atggcctgtt 120  
 tgtacattta tatctcttcc ttctagttag ctgtatttct tactttatct tcatttttgg 180  
 cacctcacag aacaaattag cccataaatt caacacctgg aggggtgtgg tttgaggagg 240  
 gatatgattt tatggagaat gatatggcaa tgtgcctaac gattttgatg aaaagtttcc 300  
 caagctactt cctacagtat tttgggtcaat atttggaatg cgtttttagtt cttcaccttt 360  
 taaattatgt cactaaactt tgtatgagtt caaataaata tttgactaaa tgtaaaatgt 420  
 ga 422

<210> 11  
 <211> 40  
 <212> PRT  
 <213> Patinopecten sp.

05647019.012601

&lt;400&gt; 11

Ser Val Ile Gln Arg Asn Ile Arg Lys Trp Val Leu Arg Leu Asn Trp  
 1 5 10 15  
 Gln Trp Trp Lys Leu Tyr Ser Lys Val Lys Pro Leu Leu Ser Ile Ala  
 20 25 30  
 Arg Gln Glu Glu Met Lys Glu  
 35 40

&lt;210&gt; 12

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 12

Leu Val Ile Gln Trp Asn Ile Arg Ala Phe Met Gly Val Lys Asn Trp  
 1 5 10 15  
 Pro Trp Met Lys Leu Tyr Phe Lys Ile Lys Pro Leu Leu Lys Ser Ala  
 20 25 30  
 Glu Thr Glu Lys Glu Met Ala Asn  
 35 40

&lt;210&gt; 13

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 13

Phe Cys Ile Gln Tyr Asn Ile Arg Ala Phe Met Asn Val Lys His Trp  
 1 5 10 15  
 Pro Trp Met Lys Leu Phe Phe Lys Ile Lys Pro Leu Leu Lys Ser Ala  
 20 25 30  
 Glu Thr Glu Lys Glu Met Ala Thr  
 35 40

&lt;210&gt; 14

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

Glu Asn Asn Val Met Asn Ile Arg Gln Phe Asn Cys Ser Pro His Pro  
 1 5 10 15  
 Tyr Trp Leu Pro Asn Phe Met Asp Val Phe Thr Trp Ser Leu Pro Phe  
 20 25 30  
 Val Gly Glu Lys Arg Val Thr Glu  
 35 40

&lt;210&gt; 15

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; consensus sequence

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(6)

09647019 012601

```
<210> 20
<211> 26
<212> PRT
<213> Apis mellifera
```

09679-03-0001

&lt;400&gt; 20

Gly	Ile	Gly	Ala	Val	Leu	Lys	Val	Leu	Thr	Thr	Gly	Leu	Pro	Ala	Leu
1				5					10					15	
Ile	Ser	Trp	Ile	Lys	Arg	Lys	Arg	Gln	Gln						
			20					25							

09642049.012601